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• (FILE 'HOME' ENTERED AT 11:06:59 ON 02 APR 2003)

FILE 'REGISTRY' ENTERED AT 11:15:56 ON 02 APR 2003
L1 1 SEA ABB=ON PLU=ON 9000-83-3/RN

FILE 'HCAPLUS' ENTERED AT 11:16:09 ON 02 APR 2003

FILE 'REGISTRY' ENTERED AT 11:16:13 ON 02 APR 2003
L2 SET SMARTSELECT ON
SEL PLU=ON L1 1- CHEM : 12 TERMS
SET SMARTSELECT OFF

FILE 'HCAPLUS' ENTERED AT 11:16:14 ON 02 APR 2003
L3 76747 SEA ABB=ON PLU=ON L2
L4 602 SEA ABB=ON PLU=ON L3 (L) (MYOSIN HEAVY CHAIN)
L5 75 SEA ABB=ON PLU=ON L4 (L) (MAN OR HUMAN)
L6 50 SEA ABB=ON PLU=ON L5 AND PD<19981105
L7 7 SEA ABB=ON PLU=ON L6 AND (DNA OR CDNA OR NUCLEIC ACID OR
NUCLEOTIDE OR POLYNUCLEOTIDE)

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WEST Search History

DATE: Wednesday, April 02, 2003

Set Name Query

side by side

Hit Count Set Name

result set

DB=USPT,PGPB; PLUR=YES; OP=ADJ

L14	L13 and l8	60	L14
L13	L12 and vector and host	141	L13
L12	L11 and (@ad<19981105)	230	L12
L11	L10 and (dna or cdna or nucleic acid or nucleotide or polynucleotide)	500	L11
L10	L9 and (human or man)	521	L10
L9	myosin heavy chain	530	L9
L8	L7 or l6 or l5 or l4 or l3 or l2 or l1	20386	L8
L7	((536/23.2)!.CCLS.)	6498	L7
L6	((435/320.1)!.CCLS.)	16086	L6
L5	((435/252.33)!.CCLS.)	2326	L5
L4	((435/252.3)!.CCLS.)	6644	L4
L3	((435/196)!.CCLS.)	671	L3
L2	((435/195)!.CCLS.)	487	L2
L1	((435/183)!.CCLS.)	2623	L1

END OF SEARCH HISTORY

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323 ... GlnLysPheHisLysLeuLeuGlnAlaPheAspIleValGlnIlePro 338
1338 ATCCACGGGG...CACAA..CTGCTCCA.GCACCGGGGACAGCCACACTTCC 1294
338 oLys...GlnHisGlnGlnAlaPheAlaLeuLeu...AlaAlaVal 352
1293 AGAAGTCCAGCATTA..GAGTCAGTCATGACACCTTGGTCTCCGCCACAG 1246
352 AlLeuTrp...LeuGlyAsnValSerPheArgValThrAsp..... 364
1245 TGCA..TGGGGGCTGGCATGGCTCAGC..CGAGTCACCACTTATGGCTGCT 1198
365 .....AsnGluAsnHisValGluValAlaAlaPglu..... 375
1197 GCCTGAGTTAGACCGGCGGACAGTGTGAGAAATGCTCGATGATGAGAGTTC 1148
376 .AlaValAlaAsnAla.....AlaMetLeu... 383
1147 AAGCTGGCTTCTCTGCTGTGTGACACCATTCAGGGAGCCCTTGGCAG 1098
384 ...MetGlyCysAsn.....ThrGluGluLeuMetValVa 394
1097 GATATGGGCTGTCCGGGCGACAGATGTGCAAGATGAAGCTTCTTACT 1048
394 LeuSerThrArgLysLeuGlnAlaGlyThrAspCysIleAla..LysLys 410
1047 A.....ACTTGTATCGTCTTACAAA 1028
411 LeuThrLeuArg.....GlnAlaThrAspMetAlaGAs 421
1027 GTTTCGGTAGAGACCCGGATGGGGAAGCCAGCAGCACTGATATG...GA 981
421 PGLYIleAlaLysPheIleTyrrAlaAsnLeuPhe...AspTrpLeuValG 437
980 TGGTCTCCAGGAGCCAGAGCCTCTCAGCTGTGACAGACCTCTCTTGG 931
437 LcIn..IleAsnIleAlaLeuGlnValGlyLysSer..... 448
930 AGAAGAGTCTGCCCTGGCTGCTGTGGCTTGTGATGACAGCGAATGTA 881
449 .....ArgThrGlyArgSerIleSerIleLeuAspI 459
880 GTGGGGGCTGTGCTGTGTAGAGCTGCACAGAGCTGCTC..... 841
459 IeTyrrGlyPheGluSerPheLysAsnAsnSerPheGluGlnPheCysIle 475
841 ..... 841
476 AsnTyrrAlaAsnGluArgLeuGln..GlnHisPheAsnArgHis..... 489
840 .....AGTAGAGCTTGAACCTTGGACACACAGGTCACACAGAGGGC 800
490 .....LeuPheLysLeuGlu 495
799 CTGCTCTGGCCAGGGGGTCTCTGGGCTCTCTCTTGGGGTAGTGA 750
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749 GAACAGAGCCCATGACAGAGGGGCTC..TGG..... 721
512 sPAsnGlnGluCysLeu...AspLeuIleGluLysLysProIleGlyLeu 527
720 .....GATTGCTGCAGAGAGCTGTGACGTCACAGTGGGATAGGCTC. 680
528 LeuSerLeuLeuAspGluLysSerAsnPheProLysAlaThrAspLeuTh 544
679 CTGTCTCTCTC..... 668
544 rPheAlaAsnLysLeuLysGlnHisLeuLysThrAsnSerCysPheLysG 561
668 ..... 668
561 LysGlnAlaArgGlyAlaPheArgValAsnHisTyrrAlaGlyValLeu 577
667 .....CACAGGGCT..GCTGTGGG 649
578 TyrrAspThrAsn..GlyPheLeuGluLysAsnAlaGAsPProLeuProAla 593
648 TACCCACAGAGCCCCGGCTAATGACACCAATGAAGTGGGCTCCCGGCT 599
594 AspLeuIleAsnLeuLeuSerSerCysAspCysGln.....LeuLeu 608
598 GAGCTTATTTGGGCCAGAGCCAGGGGCTGCCCTCCAGGAGCACTCAATGC 549
608 LysLeuPheSerThrLysMetArgGlyLysSerGlnLysProLeuMetLeu 624
548 GTGTCTGGAGCTGGCT..... 532
625 SerAspSerThrAsnGlnThrValGlyThrLysPheLysGlyGlnLeuP 641
532 ..... 532
641 eLysLeuMetAsnLysLeuGlnAsnThrSerProHisPhe.....IleA 656
531 .GCCTGCTGGGTGCATTTGAGCGGCG..ATTCCATTTATGACGAGCA 485
656 rGcys.....IleLys..ProAsnSerLysGlnLeuPro 666
484 GATGCTGATGGGCTCCCTCAATGAGATCCAAACAGGCTGCTGCTCT 435
667 ArgValTyrrGluGlu..AspLeuValLeuGlnGlnLysArgCys..... 680
434 G..GlnAGTATGATGATGAGC..A..CTCCAGGCCCTCAACTGGCTATTC 391
681 ...CysGlyValLeuGluValValArgIleSerArgSerGlyTyrrProH 696
390 TCTGCTGGGCGCTTAG..GTAGT..... 368
696 rArgLeuThrHisGlnGluPheAlaGlyArgTyrrGlyPheLeuLeuSerA 713
367 .....AAGCAC..... 362
713 sPlLysLysValAlaGlnAspProLeuSerValSerIleAlaValLeuLys 729
362 ..... 362
730 GlnTyrrAspValHisProLcInMetTyrrGlnValGlyTyrrThrLysLeuTy 746
362 ..... 362
746 rLeuArgThrGlnGlnIleGlyIlePheGluLysArgLysLysValL 763
361 .....AAATGCTGC 352
763 euGln.....GlyIleValGlyLeuGlnLysHisPheArgGlyHis 776
351 TGCACCTTCTCATTTGGCGTAGTGTGATGCADA..... 320
777 LeuSerArgAlaTyrrPheGlnAsnMetArgLysValThrLeuValLeuG 793
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793 nSerTyrrLeaArgGluAsnAlaArgArgLeuPheAspThrGlnAlaL 810
319 .....CTGTTCACAGCTGTGTGCA 301
810 Lys.....PheHisAlaAspSerValSerGluAlaSerThrAspGluLeu 824
300 GGAATGATTCAAATCC..... 284
825 SerAlaValIleHisLeuGlnSerAlaValAlaArgLysTyrrPheAlaArgL 841
283 .....ATACACATCCACAGGCTGGGAGAA..TGG..... 255
841 sHisPheAsnSerMetGlnArg.....GlnLysGluLe 852

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254	221
852	uAaGAsnValaIaTThrLysSerLysArgLysAlaGlyAArgArgIleSerG	869
			
220	GGGGAATAG.GGGACCAAGAAACCCAGGCTGGCTGGG.....	185
869	LuAspLysAspIleProLeuGlnInProGlnValGlnProThrSerMet	885
			
184	CCCCGCCAATCCCTTAT.....	167
886	SerAspLeuGlnLysArgIleLeuLysSerGlnuAaIaIaLeuSerGlnL	902
167	167
902	sGIuGlnGluAsnThrAlaLeuArgGlnInLeuArgGlnPheGlnuA	919
167	167
919	rGTPSerGluTyraSpIleLysMetLysSerMetGluLThrTrpGln	935
166			158
	ACCTGGCAG	
936	LysGlnMetSerSerLeuGlnMetSerLeuAlaIaIaArgLysSerLe	952
157	CCT.....	155
952	uAlaIaGlnSerIleThrGlnAlaGlyArgGlnAspThrSerI	969
155	155
969	IeSerProPheGlyTyraSpSerGlnuAspThrMetSerThGlyThrPro	985
			
154	GGGCATCAGCTCATG.ACACATG.....	126
986	GIuVal..ArgThr..ProThrAsnLysPheThrAsnGly.....	997
			
125	GGGGTGGCAGAACATCCCTGCCACCCCTCCACCAAGGGCTCCCAT	76
998	.AsnThrPro.....GluLeuArgIleArgGluLeuAsnGlySer	1010
			
75	CTCTACCCCATTCCTCTGTAAGCTCAAA.....	47
1011	LeuAsnAlaValaAsnIleLeuAlaArgIleuPheAspGlnArgArgLeuAs	1027
47	47
1027	nPheAspGluAspAlaArgAlaIleValaGluValLysLeuGlyProGlnA	1044
46	46
1044	IaThr.....ProAsnGlyGlnGlnGlnHisProGlu	1055
			
45	CAAGCCAGGAACCCAAATG..AAGGTATAAGACACCCAGAG	6

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OM of: US-09-830-914C-2 to: q39157.pep.* out_format : pfs
Date: Wed Apr 2 14:17:30 2003

About: Results were produced by the Gencore software, version 5.1.4_p5_4578,
Copyright (c) 1993-2003 CompuGen Ltd.

Command line parameters:
-MODE=framer-n2p.model -DEV=soft -O=US09830914C.seq -DB=q39157.pep
-SUFFIX=pts -OUT=compare2 -MISMATCH=0.1 -LOOPTC=0 -LOOPEXT=0 -UNIT=bits
-START=1 -END=1 -MATRIX=blomsum62 -TRANS=human40.cdi -LIST=45 -DOALIGN=200
-THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pfs
-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000 -NCPU=6 -NO_XLPXY
-NEG_SCORES=0 -LONGLOG -THREADS=1 -XGAPOP=10 -XGAPEXT=0.1 -FGAPOP=6
-FGAPEXT=0.1 -YGAPOP=10 -YGAPEXT=0.1 -DELOP=6 -DELEXT=0.1

Search information:

*Query=US-09-830-914C-2
Query length: 2109
Database: q39157.pep
Database sequences: 1
Database length: 1101
Search time (sec): 1

Sequence	stnd	Orig	Zscore	EScore	len	Documentation	check
q39157.pep:q39157	-	850.51	0.00	0.0	1101	TOIG of: q39157	9498
q39157.pep:q39157	-	416.20	0.00	0.0	1101	TOIG of: q39157	9498

Sequence name: q39157.pep:q39157

Sequence documentation:

TOIG of: q39157 check: 9498 from: 1 to: 1101

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; ID 039157 PRELIMINARY; PRT: 1101 AA.
; AC 039157;
; DT 01-NOV-1996 (TREMBlrel. 01, Created)
; DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
; DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
; DE Myosin (Fragment).
; GN MYOSIN HEAVY CHAIN.
; OS Arabidopsis thaliana (Mouse-ear cress).
; OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
; OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
; OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
; OC NCBI_TaxID=3702;
; RN [1]
; RP SEQUENCE FROM N.A.
; RC STRAIN=COLUMBIA ECOTYPE;
; RX MEDLINE=95111097; PubMed=7811972;
; RA Kinkema M.D., Wang H., Schlefelbein J.;
; RT "Molecular analysis of the myosin gene family of Arabidopsis
; thaliana."
; RL Plant Mol. Biol. 26:1139-1153(1994).
; DR EMBL: Z34292; CAA84065.1; -.
; DR HSSP: P08799; IMND.
; DR InterPro: IPR001609; myosin_head.
; DR InterPro: IPR004009; Myosin_N.
; DR Pfam: PF00612; IQ; 3.
; DR Pfam: PF00063; myosin_head; 1.
; DR Pfam: PF02736; Myosin_N; 1.
; DR PRINTS: PR00193; MYOSINHEAVY.
; DR PRODOM: PD000355; myosin_head; 1.
; DR SMART: SM00015; IQ; 3.
; DR SMART: SM00242; MSc; 1.
; DR PROSITE: PS50096; IQ; 1.
; FT NON_TER 1
; SQ SEQUENCE 1101 AA; 125695 MW; F9BF30291A26A184 CRC64;
;
; 039157 length: 1101 April 2, 2003 13:55 Type: P Check: 9498
; q39157

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Alignment of: US-09-830-914C-2 x q39157 ..
Alignment segment 1/1: (+)

Quality:	850.51	Score:	0
Matching length:	577	Total length:	885
Matching Percent Similarity:	75.39	Matching Percent Identity:	44.37
Total Percent Similarity:	49.15	Total Percent Identity:	28.93
Gaps:	11		

Alignment:

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4 TGCTGGGCTGTCTTCACACTTCATTGGTTCGTCCTGACG 53
||| |||||: : : : : : : : : : : : : : : |||
210 Cys..GlyValGluTyrGluLeuLysThrIleLeu 225
54 TCTACAGGGAATGGG..... 69
225 Iaphe..GlyAsnAlaLysThrSerArgAsnAlaSerSerArgPhe 241
70 .....GTACAGATGGAGCCACCTTGGGAGGTGGGAAGTAT 111
241 LylsLeuIleGluIle.....HisPheSer...AlaMetGlyLysIleC 255
112 GTTCGCC..... 119
255 YSGlYAlAlLysLeuGluThrPheLeuLysSerArgValAlaGln 271
120 .....CACACAGGTGTCAATGC 136
272 LeupheAsnGluLysArgSerTyrHisIlePheTyrGluLeuCysAlaGln 288
137 TCACTCAGGCT..... 147
288 YAlaser..ProIleLeuLysGluArgLeuLysLeuThrAlaSerGlu 304
148 .....GA 149
305 TyrThrTyrLeuSerGlnSerAspCysLeuThrIleAlaGlyValAspAs 321
150 TGCCAGGCTGCCAAGTAAAGCATTTGCAAGGCCAGCCAGCCCTGGG 199
321 PAlaGln.....LysPheHisLysLeuLeuGlnAla..... 331
200 TTCC..TTGGTCCCTATTCCCAT.....C 223
332 PheAspIleVal..GlnIleProLysGlnHisGlnGluArgAlaPheAla 348
224 TGCTCCCTGCAGTGGCCCATGGTTCCTGSCCATCTCCAGG..... 268
348 euleuAlaAlaValLeu...TyrLeu.....GlyAsnVal 358
268 ..... 268
358 IserPheArgValThrAspAsnGluAsnHisValGluValAlaAspG 375
268 ..... 268
375 LuAlaValAlaAsnAlaAlaMetLeuMetGlyCysAsnThrGluLeu 391
268 ..... 268
392 MetValValLeuSerThrArgLysLeuGlnAlaGlyThrAspCysIleAl 408
268 ..... 268
408 alyslsLeuThrLeuArgGlnAlaThrAspMetArgAspGlyIleAla 425
268 ..... 268
425 yspheIleTyrAlaAsnLeupheAspTyrLeuValGluGlnIleAsnIle 441
269 .....CTGCTGGA 276

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442 AlaLeuGluValGlyLysSerArgThrGlyArgSerIleSerIleLeuAs 458
277 TGGTATGATTTGATTCATTCTCTGACACAGTCTGGACAGCTGTGCA 326
458 PileTyrGlyPheGluSerPheLysAsnAsnSerPheGluGlnPheCys 475
327 TCAACTAGCCCAATGAGAGCTGCAGACGATTTTGTGGCTACTACTA 376
475 LeAsnTyrAlaAsnGluArgLeuGlnGlnHisPheAsnArgHisLeuPhe 491
377 AGGGCCAGAGAGAGAAATACAGCTTGAGGCTGGAGTGGTATTTCAT 426
492 LysLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 508
427 CAATTCACAGACACACAGCCCTGTGTGATCTCATGATGAGGAGACCC 476
508 LgluPheValAspAsnGlnGlnLysLeuAspLeuIleGlnLysPheI 525
477 TCAGCATCTCTCCCTCATTAATGAGGAATGCGGCTCATTCAGCCAG 526
525 LglLysLeuSerLeuLeuAspLysLeuSer.....AsnPheProLys 539
527 AGC.....GCAGCGCACTCCAGACAGCCATTTAGACTGC 561
540 AlaThrAspLeuThrPheAlaAsnLysLeuLysGlnHisLysLysThr 555
562 CTGGCAGCAGCCCTGCTGGGCCACATAAGCTCAGCCGGGAGGCCA 611
556 .....AsnSerCysPhe.....LysGlyGlnArgGlyArg 566
612 GCTTCATTTGTTGTCATTATCGGGGCTGTGGGTACACAGACAGAGC 661
566 LaphArgValAsnHisTyrAlaGlyGlnValLeuTyrAspThrAsnGly 582
662 CTGGTGAAGAAGAAAGACCTATCCCACTGAGCTGACAGAGCTCT 711
583 PheLeuGlnLysAsnArgAspProLeuProAlaAspLeuIleAsnLeu 599
712 GCAGCAATCCAGAGACCCCTGCTCATGCGGCTGTGTTCTACTAAACCA 761
599 u...SerSerCysAspCysGlnLeuLeuLysLeuPheSerThr..... 612
762 AAGAGAAGACCCAGAGAGAAACCCCTGGCCAGAGACAGGCGCTGTG 811
613 LysMetArg.....GlyLysSerGlnLysProLeuMet 623
812 .....ACCGTGGTGTCCAGTTCAAGGCTCTACT 840
624 LeuSerAspSerThrAsnGlnThrValGlyThrLysPheLysGlyGln 640
841 GGAGCAGCTTCTGAGTCTTACACAGACACAGCCCTACTATTCGCT 890
640 uPheLysLeuMetAlaLysLeuGlnLysAsnThrSerProHisPheIleArg 657
891 GCATCAAGCCCAACAGACAGGCGCAGAGCGCAGACTTTCTCAAGAGAG 940
657 LysIleLysProAsnSerLysGlnLeuProArgValTyrGlnGlnAspLeu 673
941 GTCTTCAGCAGCTGAGAGCTGTGGCTGTGGAGACCATCATATCAG 990
674 ValLeuGlnGlnLeuArgCysGlyValLeuGlnValValArgIleSer 690
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690 ArgSerGlyTyrProThrArgLeuThrHisGlnGlnPheAlaGlyArg 707
1041 ACAAGTTACTAAGAGCTTCATCTTGACATCTCTGGCCCGCAGAG 1090
707 yr.....GlyPheLeuLeuSer.....AspLys 714
1091 CCATATCTGCGCAAGAGGCTCCCTGAATGCTGTCCACACAGCGAGAGC 1140
.....
715 .....LysValAlaGlnAsp 720
1141 CAGCCTGAACCTCTCCATCCAGACATTCCTCCACACTCTGGCGTCTTA 1190
720 ro...LeuSerValSer.....IleAlaValLeu 729
1191 CTCAGGC..AGCAGCCATTACTGTGACTCGGCTGAGGCCATAGCCGCC 1239
729 LysGlnTyrAspValHis.....ProGlnMet 737
1240 CATGCACCTGTGGCAGACCAAGCTTTCAATGACTGACTATGCTGAGC 1289
737 TTYGlnValGlyTyrThrLysLeuTyrLeuArgThrGlyGlnIleGly 754
1290 TTTCCGAATGGGCGCTGCCGGGTGCTGAGCA..GTGTGCGCCCTCAT 1338
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1339 CAGAGGTGGCTGAGAGCAGACCGGCACCGAGACAGAGCGGAGCTGGC 1388
770 ..GlnLysHisPheArgGlyHisLysLeuSerArgAlaTyrPheGlnAsnMet 786
1389 GGGCGCTCATGCTCATC..... 1405
786 rGlyValThrLeuValLeuGlnSerTyrIleArgGlyGlnAsnAlaArg 802
1405 ..... 1405
803 ArgLeuPheAspThrGluAlaLysPheHisAlaAspSerValSerGluAl 819
1406 .....CAGCAGCCCTTCTGTT 1421
819 AserThrAspGluLeuSerAlaValIleHisLysGlnSerAlaValAlaArg 836
1422 CTGGTTAACTCGGAACACATC.....CAGAGCTG 1453
836 LyrThrLeuAlaArgLysHisPheAsnSerMetGlnArgGlnLysGlnLeu 852
1454 CATGCAGCTGCTCAGACATCATCAGCGT..... 1480
853 ArgAsnValAlaThrLysSerLysArgLysAlaGlyArgArgIleSerG 869
1480 ..... 1480
869 uAspLysAspIleProLeuGlnGlnProGlnValGlnProThrSerMetS 886
1480 ..... 1480
886 eAspLeuGlnLysArgIleLeuLysSerGlnAlaAlaLeuSerGlnLys 902
1481 .....GC 1482
903 GlnGlnGlnAsnThrAlaLeuArgGlnGlnLeuArgGlnPheGlnGln 919
1483 ATGGCAGAACTGAGAGATAGAAATGGGCTGCTGTGCTAAGAGCTGG 1532
919 gTPrSerGlnTyrAspIleLysMet.....LysSerMetG 931
1533 ATG..GTGTGGAAGAAACACTTCTCTCAAGCTCCCTGTGCTCCCTGAGCA 1580
931 LndLysThrTyrGlnLysGln.....MetSerSerLeu..GlnMetSer 944
1581 CTTGCGCGGTGAGACAGCCAGGCTCTGAGGACATTAATCCGCTCTGCGCC 1630
945 ..LeuAlaAlaAlaAlaArgLysSer.....LeuAla 954
1631 CTGGAGCTGTCTGAGCAATAGGCTATGAGGTGTGAGCAGCTTTCAGAG 1680
954 LndLysSerIleThrGlyGlnAlaGly...Gly..ArgGln...AspThr 967
1681 GAAATTAATGAGTCTGGGCTTGGCTTCAGAGCTCCCGAGGAGCGACCCAGTA 1730
968 SerIleSer.....ProPheGlyTyrAspSerG 977

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186 u...sergylalaglysthrleuThrAlaLysPhe.....AlaIle 199
1532 CCAGCTCTT..... 1523
199 tGlnTyrlleuAlaLalLeuGlyglYserCysGlyValGluTyrglu 216
1523 ..... 1523
216 leuLysThrThrCyslleuGluAlaPheGlyAsnAlaLysThrSer 232
1522 .....AGCAGCAGGAGGCC..ATTCTGATTCTCCACTTCT.. 1488
233 ArgAsnAlaAsnSerSerArgPheGlyLysleuIleuIleHisPhe 249
1487 ..GCCATGCA..CGCTTGATGACTGTGCAGC..... 1460
249 rAlaMetGlyLysIle...CysGlyAlaLysleuGluThrPheLeu 264
1460 ..... 1460
264 uGluLysSerArgValValGlnleuPheAsnGlyGluArgSerThrIst 281
1459 .....TGCAT..GCAGCTCTGGATGTGTTCCAG..... 1431
281 lePheTyrgluLeuCysAlaGlyAlaSerProIleuLysGluArgLeu 297
1430 .....TTACCCAGAACGAAATGGCTGC..CTGCATGACATGACGGCCC 1389
298 LysleuLysThrAlaSerGluTyrlThrTyrlleuSerIleSerAp... 312
1388 GCACACTGGCCGCTCTCGGTGGTGGCTGCCTCCAGCCACCTGG 1339
313 .....Cys..LeuThrIle...AlaGlyAlaAspAspAla..... 322
1338 ATGCAGCGGG..CACA..CTGCTGCA..GCACCGGGGACGCCACATTC 1294
323 ..GlnLysPheHisLysleuLeuGluAlaPheAspIleValGlnIlePr 338
1293 AGAACCTCCAGATG..GAGTCAGTCAGAACACTGTGCTCGTCAGAC 1246
338 Olys...GlnHisGlnleuArgAlaPheAlaLeuLeu...AlaAlaV 352
1245 TSCA..TGGGGGCTGGCATGGCTCAGC..CGAGTCACCAATTATGGCTCT 1198
352 alLeuTrp..LeuGlyAsnValSerPheArgValThrAsp..... 364
1197 GCCTGAGTTAGGACCGGAGAGTGGAGAAATGCTCTGATGAGAGTTC 1148
365 .....AsnGlnAsnHisValGluValAlaAlaAspGlu..... 375
1147 AAGCGTGGCTTCCTCGCTGTGTGACACCATTCAGGGAGCCCTTGGCAG 1098
376 ..AlaValAlaAsnAla.....AlaMetLeu... 383
1097 GATATGGGCTGTGGGGCCAGAGATGTCAAGATGAAGACTTCTTACT 1048
384 ...MetGlyCysAsn.....ThrGluGluLeuMetValVa 394
1047 A.....ACTGTATCGTTCTACAA 1028
394 lleuSerThrArgLysleuGlnAlaGlyThrAspCysIleAla..LysLys 410
1027 GTTTCGGTGAAGACCCGATGGGGAAGCCAGACAGCATGATATG...GA 981
411 leuThrLeuArg.....GlnAlaThrAspMetArgAs 421
980 TGGTCTCCAGAGCCACAGGCTCCAGCTGAGCTGAGACCTCTCTGG 931
421 pGlyIleAlaLysPheIleTyrlAlaAsnleuPhe...AspTrpLeuValG 437
930 AGAAAGTCTGGCGCTGGCCCTGCTGTTGGCTGTGATGACAGGATGTA 881

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437 IuGln...IleAsnIleAlaLeuGluValGlyLysSer..... 448
880 GTGGGGCTGTGCTGTCTGTACGACCTGCAGAGCTGCTCC..... 841
449 .....ArgThrGlyArgSerIleSerIleLeuAspI 459
841 ..... 841
459 leTyrglyPheGluSerPheLysAsnAsnSerPheGluGlnPheCysIle 475
840 .....AGTAGCCCTTGAACTTGACACACACGCGTCAACAGAGGCC 800
476 AsnTyrlAlaAsnGluArgLeuGln..GlnHisPheAsnArgHis..... 489
799 CCTGCTCGGCCAGAGGGGTTCTCTCGGTGCTCTCTTGGGTTAGTAG 750
490 .....LeuPheLysleuGluG 495
749 GAACAGCCCCATGAGACAGGGGCTC..TGG..... 721
495 nGluGluTyrgluGluAspGlyIleAspTrpThrLysValGluPheVal 512
720 .....GATGCTGCAGAGCCTGTCAGCTCAGCTGCGATAGGATC 680
512 spAsnGlnIuLysLeu...AspLeuIleGluLysLysProIleGlyLeu 527
679 CTGTGTTCTTCTC..... 668
528 leuSerLeuLeuAspGluGluSerAsnPheProLysAlaThrAspLeuTh 544
668 ..... 668
544 rPheAlaAsnLysLeuLysGlnHisLeuLysThrAsnSerCysPheLysG 561
667 .....CACCAGGCTC..CCTGTGG 649
561 LysLysArgGlyArgAlaPheArgValAsnHisTyrlAlaGlyLysValLeu 577
648 TACCCGACAGGCCCCGATATATGACCCACAAATGAACTGGCTCCGGCT 599
578 TyrAspThrAsn..GlyPheLeuGlnLysAsnArgspProleuProAla 593
598 GAGCTATGTTGGCCGACGAGGAGGCTGCTGCACGAGTCTCAATGC 549
594 AspLeuIleAsnleuLeuSerSerCysAspCysGln.....LeuLeuL 608
548 GTGTCTGGAGCTGGCT..... 532
608 LysleuPheSerThrLysMetArgGlyLysSerGlnLysProleuMetLeu 624
532 ..... 532
625 SerAspSerThrAsnGlnThrValGlyThrLysPheLysGlyGlnleuTh 641
531 ..GCCTGCTGGTGCATGAGGGGCC..ATTCTCATTTATGAGGAGCA 485
641 elYsleuMetAsnLysleuGlnAsnThrSerProHisPhe.....IleA 656
484 GATCTGATGGGCTTCCCTCAATGAGATGCCAAACAGGCGCTGGTGGCT 435
656 rGcys.....IleLys..ProAsnSerLysGlnleuPro 666
434 G..GTAGTGATGAATGACC..A..CTCCAGGCCCTCAACTGCGTATTC 391
667 ArgValLysTrpGluGln..AspLeuValLysleuGlnleuAlaGcys..... 680
390 TCTGCTGGGCGCTTAG..GTAGTG..... 368
681 ...CysGlyValLysleuGluValAlaArgIleSerArgSerGlyTyrlProth 696
368 ..... 368
696 rArgleuThrHisGlnleuPheAlaGlyArgTyrglyPheleuLeuSerA 713

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368 ..... 368
713 splyslyValAlaGlnaspProleuSerValSerIleAlaValLeuLys 729
368 ..... 368
730 GluTyrAspValHisProGluMetTyrGlnValGlyTyrThrLysLeuTy 746
367 ..... AGCCACAAATGCTGC 352
746 rleuArgThrGlyGlnIleGlyIlePheGluAspArgArgLysLysValL 763
351 TGCAGCTTCATTCATGGCGTAGTTGATGCACA ..... 320
763 eugIn ..... GlyIleValGlyLeuGlnLysHisPheArgGlyHis 776
320 ..... 320
777 leuSerArgAlaTyrPheGlnAsnMetArgLysValThrLeuValLeuG 793
319 ..... CTGTCAGACTGTGTCA 301
793 nSerTyrIleArgGlyGluAsnAlaArgArgLeuPheAspThrGluAlaL 810
300 GGAATGATTCAATCC ..... 284
810 ys ..... PheHisAlaAspSerValSerGluAlaSerThrAspGluLeu 824
283 ..... ATACATCCACAGCGCTGGAGACA.TGG ..... 255
825 SerAlaValIleHisLeuGlnSerAlaValArgGlyTyrPleuAlaArgLy 841
254 ..... CAGAAACCATGGGCGCACGTCAGGAGCAGAT 221
841 SHSPheAsnSerMetGlnArg ..... GlnLysGluLe 852
220 GCGGAATAG.GCGACCAAGAACCCAGGTGCTGG ..... 185
852 uArgAsnValAlaThrLysSerLysArgLysAlaGlyArgArgIleSerG 869
184 ..... CCCCTGCCAATGCCCTTAT ..... 167
869 LysAspLysAspIleProLeuGlnGlnProGlnValGlnProThrSerMet 885
167 ..... 167
886 SerAspLeuGlnLysArgIleLeuLysSerGluAlaAlaLeuSerGlnLy 902
167 ..... 167
902 sGluGluGluAsnThrAlaLeuArgGluGlnLeuArgGlnPheGluGlu 919
166 ..... ACTTGGCAG 158
919 rGtrPserGluTyrAspIleLysMetLysSerMetGluGluThrTrpGln 935
157 CCT ..... 155
936 LysGlnMetSerSerLeuGlnMetSerLeuAlaAlaArgLysSerLe 952
155 ..... 155
952 uAlaAlaGluSerIleThrGlyGlnAlaGlyLysArgLysAspThrSerI 969
154 ..... GGCATCAGGCTGAGTG.AGCATG ..... ACACCT 126
969 leSerProPheGlyTyrAspSerGluAspThrMetSerThrGlyThrPro 985
125 GTGGTGGCAGACATACCTCCACACCTCCACCAAGTGGCTCCCAT 76
986 GlyVal...ArgThr...ProThrAsnLysPheThrAsnGly ..... 997

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75 CTCTACCCCAATTCCCTGTAGAGCTCAGA ..... 47
998 .AsnThrPro ..... GluLeuArgIleArgGluLeuAsnGlySer 1010
47 ..... 47
1011 leuAsnAlaValAsnHisLeuAlaArgGluPheAspGlnArgArgLeuAs 1027
46 .....G 46
1027 nPheAspGluAspAlaArgAlaIleValGluValLysLeuGlyProGlnA 1044
45 CAAGCAGGAAACCCAAATG..AAGTGTGAAGACAGCCCGAG 6
1044 latr ..... ProAsnGlyGlnGlnGlnHisProGlu 1055

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